RAW SEQUENCE LISTING ERROR REPORT
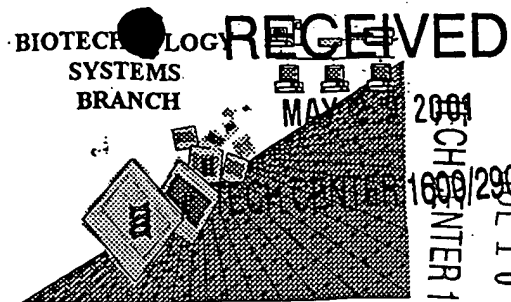
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/746,371A_

Source: _1600_

Date Processed by STIC: _5/10/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:


Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker
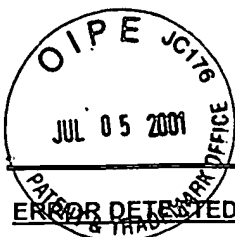
Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED CORRECTION   SERIAL NUMBER: ___09/746,371A___

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid
Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of "Artificial"
(NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature
(NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/746,371A

DATE: 05/10/2001
TIME: 12:21:36

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**Does Not Comply
Corrected Diskette Needed**

Input Set : A:\BERL025.txt
Output Set: N:\CRF3\05102001\I746371A.raw

```
  3 <110> APPLICANT: Urry, Dan
  5 <120> TITLE OF INVENTION: Acoustic Absorption Polymers and Their Methods of Use
  7 <130> FILE REFERENCE: BERL025/01US
  9 <140> CURRENT APPLICATION NUMBER: 09/746371A
 10 <141> CURRENT FILING DATE: 2000-12-20
 12 <160> NUMBER OF SEQ ID NOS: 47
 14 <170> SOFTWARE: PatentIn version 3.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 5
 18 <212> TYPE: PRT
C--> 19 <213> ORGANISM: Artificial          (global error)  see item 11 on Error Summary Sheet
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: This is a synthetic sequence.
 24 <220> FEATURE:
 25 <221> NAME/KEY: PEPTIDE
 26 <222> LOCATION: (1)..(5)
 28 <400> SEQUENCE: 1
 30 Val Pro Gly Val Gly
 31 1               5
 33 <210> SEQ ID NO: 2
 34 <211> LENGTH: 4
 35 <212> TYPE: PRT
C--> 36 <213> ORGANISM: Artificial
 38 <220> FEATURE:
 39 <223> OTHER INFORMATION: This is a synthetic sequence.
 41 <220> FEATURE:
 42 <221> NAME/KEY: PEPTIDE
 43 <222> LOCATION: (1)..(4)
 45 <400> SEQUENCE: 2
 47 Val Pro Gly Gly
 48 1
 50 <210> SEQ ID NO: 3
 51 <211> LENGTH: 4
 52 <212> TYPE: PRT
C--> 53 <213> ORGANISM: Artificial
 55 <220> FEATURE:
 56 <223> OTHER INFORMATION: This is a synthetic sequence.
 58 <220> FEATURE:
 59 <221> NAME/KEY: PEPTIDE
 60 <222> LOCATION: (1)..(4)
 62 <400> SEQUENCE: 3
 64 Gly Gly Val Pro
 65 1
 67 <210> SEQ ID NO: 4
 68 <211> LENGTH: 4
 69 <212> TYPE: PRT
C--> 70 <213> ORGANISM: Artificial
```

RAW SEQUENCE LISTING   DATE: 05/10/2001
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Input Set : A:\BERL025.txt
Output Set: N:\CRF3\05102001\I746371A.raw

```
 72 <220> FEATURE:
 73 <223> OTHER INFORMATION: This is a synthetic sequence.
 75 <220> FEATURE:
 76 <221> NAME/KEY: PEPTIDE
 77 <222> LOCATION: (1)..(4)
 79 <400> SEQUENCE: 4
 81 Gly Gly Phe Pro
 82 1
 84 <210> SEQ ID NO: 5
 85 <211> LENGTH: 4
 86 <212> TYPE: PRT
C--> 87 <213> ORGANISM: Artificial
 89 <220> FEATURE:
 90 <223> OTHER INFORMATION: This is a synthetic sequence.
 92 <220> FEATURE:
 93 <221> NAME/KEY: PEPTIDE
 94 <222> LOCATION: (1)..(4)
 96 <400> SEQUENCE: 5
 98 Gly Gly Ala Pro
 99 1
101 <210> SEQ ID NO: 6
102 <211> LENGTH: 5
103 <212> TYPE: PRT
C--> 104 <213> ORGANISM: Artificial
106 <220> FEATURE:
107 <223> OTHER INFORMATION: This is a synthetic sequence.
109 <220> FEATURE:
110 <221> NAME/KEY: VARIANT
111 <222> LOCATION: (2)..(4)
112 <223> OTHER INFORMATION: Residue at position 2 is V, E, F, Y or K
113        Residue at position 4 is V, E, F or I
116 <400> SEQUENCE: 6
118 Gly Xaa Gly Xaa Pro
119 1              5
121 <210> SEQ ID NO: 7
122 <211> LENGTH: 6
123 <212> TYPE: PRT
C--> 124 <213> ORGANISM: Artificial
126 <220> FEATURE:
127 <223> OTHER INFORMATION: This is a synthetic sequence.
129 <220> FEATURE:
130 <221> NAME/KEY: PEPTIDE
131 <222> LOCATION: (1)..(6)
133 <400> SEQUENCE: 7
135 Ala Pro Gly Val Gly Val
136 1              5
138 <210> SEQ ID NO: 8
139 <211> LENGTH: 35
140 <212> TYPE: PRT
```

```
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                    Input Set : A:\BERL025.txt
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C--> 141 <213> ORGANISM: Artificial
     143 <220> FEATURE:
     144 <223> OTHER INFORMATION: This is a synthetic sequence.
     146 <220> FEATURE:
     147 <221> NAME/KEY: PEPTIDE
     148 <222> LOCATION: (1)..(35)
     150 <400> SEQUENCE: 8
     152 Gly Val Gly Val Pro Gly Val Gly Phe Pro Gly Glu Gly Phe Pro Gly
     153 1               5                   10                  15
     155 Val Gly Val Pro Gly Val Gly Phe Pro Gly Phe Gly Phe Pro Gly Val
     156             20                  25                  30
     158 Gly Val Pro
     159         35
     161 <210> SEQ ID NO: 9
     162 <211> LENGTH: 35
     163 <212> TYPE: PRT
C--> 164 <213> ORGANISM Artificial
     166 <220> FEATURE:
     167 <223> OTHER INFORMATION: This is a synthetic sequence.
     169 <220> FEATURE:
     170 <221> NAME/KEY: PEPTIDE
     171 <222> LOCATION: (1)..(35)
     173 <400> SEQUENCE: 9
     175 Gly Val Gly Val Pro Gly Val Gly Phe Pro Gly Glu Gly Phe Pro Gly
     176 1               5                   10                  15
     178 Val Gly Val Pro Gly Val Gly Phe Pro Gly Val Gly Phe Pro Gly Val
     179             20                  25                  30
     181 Gly Val Pro
     182         35
     184 <210> SEQ ID NO: 10
     185 <211> LENGTH: 35
     186 <212> TYPE: PRT
C--> 187 <213> ORGANISM: Artificial
     189 <220> FEATURE:
     190 <223> OTHER INFORMATION: This is a synthetic sequence.
     192 <220> FEATURE:
     193 <221> NAME/KEY: PEPTIDE
     194 <222> LOCATION: (1)..(35)
     196 <400> SEQUENCE: 10
     198 Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Glu Gly Val Pro Gly
     199 1               5                   10                  15
     201 Val Gly Val Pro Gly Val Gly Phe Pro Gly Phe Gly Phe Pro Gly Val
     202             20                  25                  30
     204 Gly Val Pro
     205         35
     207 <210> SEQ ID NO: 11
     208 <211> LENGTH: 35
     209 <212> TYPE: PRT
C--> 210 <213> ORGANISM Artificial
```

```
212 <220> FEATURE:
213 <223> OTHER INFORMATION: This is a synthetic sequence.
215 <220> FEATURE:
216 <221> NAME/KEY: PEPTIDE
217 <222> LOCATION: (1)..(35)
219 <400> SEQUENCE: 11
221 Gly Val Gly Val Pro Gly Val Gly Phe Pro Gly Glu Gly Phe Pro Gly
222 1               5                   10                  15
224 Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val
225             20              25              30
227 Gly Val Pro
228         35
230 <210> SEQ ID NO: 12
231 <211> LENGTH: 35
232 <212> TYPE: PRT
C--> 233 <213> ORGANISM: Artificial
235 <220> FEATURE:
236 <223> OTHER INFORMATION: This is a synthetic sequence.
238 <220> FEATURE:
239 <221> NAME/KEY: PEPTIDE
240 <222> LOCATION: (1)..(35)
242 <400> SEQUENCE: 12
244 Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Glu Gly Val Pro Gly
245 1               5                   10                  15
247 Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val
248             20              25              30
250 Gly Val Pro
251         35
253 <210> SEQ ID NO: 13
254 <211> LENGTH: 65
255 <212> TYPE: PRT
C--> 256 <213> ORGANISM: Artificial
258 <220> FEATURE:
259 <223> OTHER INFORMATION: This is a synthetic sequence.
261 <220> FEATURE:
262 <221> NAME/KEY: PEPTIDE
263 <222> LOCATION: (1)..(65)
265 <400> SEQUENCE: 13
267 Gly Val Gly Ile Pro Gly Phe Gly Glu Pro Gly Glu Gly Phe Pro Gly
268 1               5                   10                  15
270 Val Gly Val Pro Gly Phe Gly Phe Pro Gly Phe Gly Ile Pro Gly Val
271             20              25              30
273 Gly Ile Pro Gly Phe Gly Glu Pro Gly Glu Gly Phe Pro Gly Val Gly
274         35              40              45
276 Val Pro Gly Phe Gly Phe Pro Gly Phe Gly Ile Pro Gly Val Gly Val
277     50              55              60
279 Pro
280 65
282 <210> SEQ ID NO: 14
```

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Input Set : A:\BERL025.txt
Output Set: N:\CRF3\05102001\I746371A.raw

```
      283 <211> LENGTH: 35
      284 <212> TYPE: PRT
C--> 285 <213> ORGANISM: Artificial
      287 <220> FEATURE:
      288 <223> OTHER INFORMATION: This is a synthetic sequence.
      290 <220> FEATURE:
      291 <221> NAME/KEY: PEPTIDE
      292 <222> LOCATION: (1)..(35)
      294 <400> SEQUENCE: 14
      296 Gly Val Gly Val Pro Gly Val Gly Phe Pro Gly Lys Gly Phe Pro Gly
      297 1               5                   10                  15
      299 Val Gly Val Pro Gly Val Gly Phe Pro Gly Phe Gly Phe Pro Gly Val
      300             20                  25                  30
      302 Gly Val Pro
      303         35
      305 <210> SEQ ID NO: 15
      306 <211> LENGTH: 35
      307 <212> TYPE: PRT
C--> 308 <213> ORGANISM: Artificial
      310 <220> FEATURE:
      311 <223> OTHER INFORMATION: This is a synthetic sequence.
      313 <220> FEATURE:
      314 <221> NAME/KEY: PEPTIDE
      315 <222> LOCATION: (1)..(35)
      317 <400> SEQUENCE: 15
      319 Gly Val Gly Val Pro Gly Val Gly Phe Pro Gly Lys Gly Phe Pro Gly
      320 1               5                   10                  15
      322 Val Gly Val Pro Gly Val Gly Phe Pro Gly Val Gly Phe Pro Gly Val
      323             20                  25                  30
      325 Gly Val Pro
      326         35
      328 <210> SEQ ID NO: 16
      329 <211> LENGTH: 35
      330 <212> TYPE: PRT
C--> 331 <213> ORGANISM: Artificial
      333 <220> FEATURE:
      334 <223> OTHER INFORMATION: This is a synthetic sequence.
      336 <220> FEATURE:
      337 <221> NAME/KEY: PEPTIDE
      338 <222> LOCATION: (1)..(35)
      340 <400> SEQUENCE: 16
      342 Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Lys Gly Val Pro Gly
      343 1               5                   10                  15
      345 Val Gly Val Pro Gly Val Gly Phe Pro Gly Phe Gly Phe Pro Gly Val
      346             20                  25                  30
      348 Gly Val Pro
      349         35
      351 <210> SEQ ID NO: 17
      352 <211> LENGTH: 35
```

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Please Note:
Use f n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing t ensure that a c rresp nding explanati n is presented in the <220> to <223> fields of each sequence which presents at least ne n or Xaa.

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Input Set : A:\BERL025.txt
Output Set: N:\CRF3\05102001\I746371A.raw

```
L:19  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:36  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:53  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:70  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:87  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:104 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:124 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:141 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:164 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:187 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:210 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:233 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:256 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:285 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:308 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:331 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:354 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:377 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:400 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:423 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:446 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:466 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:483 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:502 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:517 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:523 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:543 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:561 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:579 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:596 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:619 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:639 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:659 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:682 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:702 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:722 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35
L:757 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36
L:794 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:37
L:820 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38
L:848 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39
L:871 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40
L:894 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41
L:914 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42
L:936 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:43
L:953 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:44
```

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L:972 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:45
L:989 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:46
L:1008 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47